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1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/037,182

DATE: 02/07/2002

TIME: 18:38:43

Input Set : A:\99274Fseq.txt

Output Set: N:\CRF3\02072002\J037182.raw

3 <110> APPLICANT: Tryggvason, Karl
4 Doi, Masayuki
5 Thyboll, Jill
7 <120> TITLE OF INVENTION: Recombinant Laminin 10
9 <130> FILE REFERENCE: 99-274-F
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/037,182
C--> 12 <141> CURRENT FILING DATE: 2001-12-21
14 <150> PRIOR APPLICATION NUMBER: 60/257,449
15 <151> PRIOR FILING DATE: 2000-12-21
17 <150> PRIOR APPLICATION NUMBER: 60/279,282
18 <151> PRIOR FILING DATE: 2001-03-28
20 <160> NUMBER OF SEQ ID NOS: 36
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 11350
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (68)..(11152)
33 <220> FEATURE:
34 <221> NAME/KEY: sig_peptide
35 <222> LOCATION: (68)..(173)
37 <400> SEQUENCE: 1

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40 cgggaag atg gcg aag cgg ctc tgc gcg ggg agc gca ctg tgt gtt cgc 109
41 Met Ala Lys Arg Leu Cys Ala Gly Ser Ala Leu Cys Val Arg
42 1 5 10
44 ggc ccc cgg ggc ccc gcg ccg ctg ctg ctg gtc ggg ctg gcg ctg ctg 157
45 Gly Pro Arg Gly Pro Ala Pro Leu Leu Leu Val Gly Leu Ala Leu Leu
46 15 20 25 30
48 ggc gcg gcg cgg gcg cgg gag gag gcg ggc ggc ggc ttc agc ctg cac 205
49 Gly Ala Ala Arg Ala Arg Glu Glu Ala Gly Gly Gly Phe Ser Leu His
50 35 40 45
52 ccg ccc tac ttc aac ctg gcc gag ggc gcc cgc atc gcc gcc tcc gcg 253
53 Pro Pro Tyr Phe Asn Leu Ala Glu Gly Ala Arg Ile Ala Ala Ser Ala
54 50 55 60
56 acc tgc gga gag gag gcc ccg gcg cgc ggc tcc ccg cgc ccc acc gag 301
57 Thr Cys Gly Glu Glu Ala Pro Ala Arg Gly Ser Pro Arg Pro Thr Glu
58 65 70 75
60 gac ctt tac tgc aag ctg gta ggg ggc ccc gtg gcc ggc ggc gac ccc 349
61 Asp Leu Tyr Cys Lys Leu Val Gly Gly Pro Val Ala Gly Gly Asp Pro
62 80 85 90

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64	aac	cag	acc	atc	cgg	ggc	cag	tac	tgc	gac	atc	tgc	acg	gct	gcc	aac	397
65	Asn	Gln	Thr	Ile	Arg	Gly	Gln	Tyr	Cys	Asp	Ile	Cys	Thr	Ala	Ala	Asn	
66	95					100				105						110	
68	agc	aac	aag	gca	cac	ccc	gcg	agc	aat	gcc	atc	gat	ggc	acg	gag	cgc	445
69	Ser	Asn	Lys	Ala	His	Pro	Ala	Ser	Asn	Ala	Ile	Asp	Gly	Thr	Glu	Arg	
70					115					120						125	
72	tgg	tgg	cag	agt	cca	ccg	ctg	tcc	cgc	ggc	ctg	gag	tac	aac	gag	gtc	493
73	Trp	Trp	Gln	Ser	Pro	Pro	Leu	Ser	Arg	Gly	Leu	Glu	Tyr	Asn	Glu	Val	
74					130					135						140	
76	aac	gtc	acc	ctg	gac	ctg	ggc	cag	gtc	ttc	cac	gtg	gcc	tac	gtc	ctc	541
77	Asn	Val	Thr	Leu	Asp	Leu	Gly	Gln	Val	Phe	His	Val	Ala	Tyr	Val	Leu	
78					145					150						155	
80	atc	aag	ttt	gcc	aac	tca	ccc	cgg	ccg	gac	ctc	tgg	gtg	ctg	gag	cgg	589
81	Ile	Lys	Phe	Ala	Asn	Ser	Pro	Arg	Pro	Asp	Leu	Trp	Val	Leu	Glu	Arg	
82					160					165						170	
84	tcc	atg	gac	ttc	ggc	cgc	acc	tac	cag	ccc	tgg	cag	ttc	ttt	gcc	tcc	637
85	Ser	Met	Asp	Phe	Gly	Arg	Thr	Tyr	Gln	Pro	Trp	Gln	Phe	Phe	Ala	Ser	
86	175					180				185						190	
88	tct	aag	agg	gac	tgt	ctg	gag	cgg	ttc	ggg	cca	cag	acg	ctg	gag	cgc	685
89	Ser	Lys	Arg	Asp	Cys	Leu	Glu	Arg	Phe	Gly	Pro	Gln	Thr	Leu	Glu	Arg	
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92	atc	aca	cgg	gac	gac	gca	gcc	atc	tgc	acc	acc	gag	tac	tca	cgc	atc	733
93	Ile	Thr	Arg	Asp	Asp	Ala	Ala	Ile	Cys	Thr	Thr	Glu	Tyr	Ser	Arg	Ile	
94					210					215						220	
96	gtg	ccc	ctg	gag	aac	gga	gag	atc	gtg	gtg	tcc	ctg	gtg	aac	gga	cgt	781
97	Val	Pro	Leu	Glu	Asn	Gly	Glu	Ile	Val	Val	Ser	Leu	Val	Asn	Gly	Arg	
98					225					230						235	
100	ccg	ggc	gcc	atg	aat	ttc	tcc	tac	tcg	ccg	ctg	cta	cgt	gag	ttc	acc	829
101	Pro	Gly	Ala	Met	Asn	Phe	Ser	Tyr	Ser	Pro	Leu	Leu	Arg	Glu	Phe	Thr	
102					240					245						250	
104	aag	gcc	acc	aac	gtc	cgc	ctg	cgc	ttc	ctg	cgt	acc	aac	acg	ctg	ctg	877
105	Lys	Ala	Thr	Asn	Val	Arg	Leu	Arg	Phe	Leu	Arg	Thr	Asn	Thr	Leu	Leu	
106	255					260				265						270	
108	ggc	cat	ctc	atg	ggg	aag	gcg	ctg	cgg	gac	ccc	acg	gtc	acc	cgc	cgg	925
109	Gly	His	Leu	Met	Gly	Lys	Ala	Leu	Arg	Asp	Pro	Thr	Val	Thr	Arg	Arg	
110					275					280						285	
112	tat	tat	tac	agc	atc	aag	gat	atc	agc	atc	gga	ggc	cgc	tgt	gtc	tgc	973
113	Tyr	Tyr	Tyr	Ser	Ile	Lys	Asp	Ile	Ser	Ile	Gly	Gly	Arg	Cys	Val	Cys	
114					290					295						300	
116	cac	ggc	cac	gcg	gat	gcc	tgc	gat	gcc	aaa	gac	ccc	acg	gac	ccg	ttc	1021
117	His	Gly	His	Ala	Asp	Ala	Cys	Asp	Ala	Lys	Asp	Pro	Thr	Asp	Pro	Phe	
118					305					310						315	
120	agg	ctg	cag	tgc	acc	tgc	cag	cac	aac	acc	tgc	ggg	ggc	acc	tgc	gac	1069
121	Arg	Leu	Gln	Cys	Thr	Cys	Gln	His	Asn	Thr	Cys	Gly	Gly	Thr	Cys	Asp	
122					320					325						330	
124	cgc	tgc	tgc	ccc	ggc	ttc	aat	cag	cag	ccg	tgg	aag	cct	gcg	act	gcc	1117
125	Arg	Cys	Cys	Pro	Gly	Phe	Asn	Gln	Gln	Pro	Trp	Lys	Pro	Ala	Thr	Ala	
126	335					340				345						350	
128	aac	agt	gcc	aac	gag	tgc	cag	tcc	tgt	aac	tgc	tac	ggc	cat	gcc	acc	1165

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129	Asn	Ser	Ala	Asn	Glu	Cys	Gln	Ser	Cys	Asn	Cys	Tyr	Gly	His	Ala	Thr	
130					355					360					365		
132	gac	tgt	tac	tac	gac	cct	gag	gtg	gac	cgg	cgc	cgc	gcc	agc	cag	agc	1213
133	Asp	Cys	Tyr	Tyr	Asp	Pro	Glu	Val	Asp	Arg	Arg	Arg	Ala	Ser	Gln	Ser	
134					370					375					380		
136	ctg	gat	ggc	acc	tat	cag	ggt	ggg	ggt	gtc	tgt	atc	gac	tgc	cag	cac	1261
137	Leu	Asp	Gly	Thr	Tyr	Gln	Gly	Gly	Gly	Val	Cys	Ile	Asp	Cys	Gln	His	
138					385					390					395		
140	cac	acc	gcc	ggc	gtc	aac	tgt	gag	cgc	tgc	ctg	ccc	ggc	ttc	tac	cgc	1309
141	His	Thr	Ala	Gly	Val	Asn	Cys	Glu	Arg	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	
142		400					405					410					
144	tct	ccc	aac	cac	cct	ctc	gac	tcg	ccc	cac	gtc	tgc	cgc	cgc	tgc	aac	1357
145	Ser	Pro	Asn	His	Pro	Leu	Asp	Ser	Pro	His	Val	Cys	Arg	Arg	Cys	Asn	
146	415					420					425					430	
148	tgc	gag	tcc	gac	ttc	acg	gat	ggc	acc	tgc	gag	gac	ctg	acg	ggt	cga	1405
149	Cys	Glu	Ser	Asp	Phe	Thr	Asp	Gly	Thr	Cys	Glu	Asp	Leu	Thr	Gly	Arg	
150					435					440					445		
152	tgc	tac	tgc	cgg	ccc	aac	ttc	tct	ggg	gag	cgg	tgt	gac	gtg	tgt	gcc	1453
153	Cys	Tyr	Cys	Arg	Pro	Asn	Phe	Ser	Gly	Glu	Arg	Cys	Asp	Val	Cys	Ala	
154					450					455					460		
156	gag	ggc	ttc	acg	ggc	ttc	cca	agc	tgc	tac	ccg	acg	ccc	tcg	tcc	tcc	1501
157	Glu	Gly	Phe	Thr	Gly	Phe	Pro	Ser	Cys	Tyr	Pro	Thr	Pro	Ser	Ser	Ser	
158					465					470					475		
160	aat	gac	acc	agg	gag	cag	gtg	ctg	cca	gct	ggc	cag	att	gtg	aat	tgt	1549
161	Asn	Asp	Thr	Arg	Glu	Gln	Val	Leu	Pro	Ala	Gly	Gln	Ile	Val	Asn	Cys	
162		480					485					490					
164	gac	tgc	agc	gcg	gca	ggg	acc	cag	ggc	aac	gcc	tgc	cgg	aag	gac	cca	1597
165	Asp	Cys	Ser	Ala	Ala	Gly	Thr	Gln	Gly	Asn	Ala	Cys	Arg	Lys	Asp	Pro	
166	495					500				505					510		
168	agg	gtg	gga	cgc	tgt	ctg	tgc	aaa	ccc	aac	ttc	caa	ggc	acc	cat	tgt	1645
169	Arg	Val	Gly	Arg	Cys	Leu	Cys	Lys	Pro	Asn	Phe	Gln	Gly	Thr	His	Cys	
170					515					520					525		
172	gag	ctc	tgc	gcg	cca	ggg	ttc	tac	ggc	ccc	ggc	tgc	cag	ccc	tgc	cag	1693
173	Glu	Leu	Cys	Ala	Pro	Gly	Phe	Tyr	Gly	Pro	Gly	Cys	Gln	Pro	Cys	Gln	
174					530					535					540		
176	tgt	tcc	agc	cct	gga	gtg	gcc	gat	gac	cgc	tgt	gac	cct	gac	aca	ggc	1741
177	Cys	Ser	Ser	Pro	Gly	Val	Ala	Asp	Asp	Arg	Cys	Asp	Pro	Asp	Thr	Gly	
178					545					550					555		
180	cag	tgc	agg	tgc	cga	gtg	ggc	ttc	gag	ggg	gcc	aca	tgt	gat	cgc	tgt	1789
181	Gln	Cys	Arg	Cys	Arg	Val	Gly	Phe	Glu	Gly	Ala	Thr	Cys	Asp	Arg	Cys	
182					560					565					570		
184	gcc	ccc	ggc	tac	ttt	cac	ttc	cct	ctc	tgc	cag	ttg	tgt	ggc	tgc	agc	1837
185	Ala	Pro	Gly	Tyr	Phe	His	Phe	Pro	Leu	Cys	Gln	Leu	Cys	Gly	Cys	Ser	
186	575					580				585					590		
188	cct	gca	gga	acc	ttg	ccc	gag	ggc	tgc	gat	gag	gcc	ggc	cgc	tgc	cta	1885
189	Pro	Ala	Gly	Thr	Leu	Pro	Glu	Gly	Cys	Asp	Glu	Ala	Gly	Arg	Cys	Leu	
190					595					600					605		
192	tgc	cag	cct	gag	ttt	gct	gga	cct	cat	tgt	gac	cgg	tgc	cgc	cct	ggc	1933
193	Cys	Gln	Pro	Glu	Phe	Ala	Gly	Pro	His	Cys	Asp	Arg	Cys	Arg	Pro	Gly	

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197	Tyr His Gly Phe Pro Asn Cys Gln Ala Cys Thr Cys Asp Pro Arg Gly						
198		625		630		635	
200	gcc ctg gac cag ctc tgt ggg gcg gga ggt ttg tgc cgc tgc cgc ccc	2029					
201	Ala Leu Asp Gln Leu Cys Gly Ala Gly Gly Leu Cys Arg Cys Arg Pro						
202		640		645		650	
204	ggc tac aca ggc act gcc tgc cag gaa tgc agc ccc ggc ttt cac ggc	2077					
205	Gly Tyr Thr Gly Thr Ala Cys Gln Glu Cys Ser Pro Gly Phe His Gly						
206	655		660		665		670
208	ttc ccc agc tgt gtc ccc tgc cac tgc tct gct gaa ggc tcc ctg cac	2125					
209	Phe Pro Ser Cys Val Pro Cys His Cys Ser Ala Glu Gly Ser Leu His						
210		675		680		685	
212	gca gcc tgt gac ccc cgg agt ggg cag tgc agc tgc cgg ccc cgt gtg	2173					
213	Ala Ala Cys Asp Pro Arg Ser Gly Gln Cys Ser Cys Arg Pro Arg Val						
214		690		695		700	
216	acg ggg ctg cgg tgt gac acg tgt gtg ccc ggt gcc tac aac ttc ccc	2221					
217	Thr Gly Leu Arg Cys Asp Thr Cys Val Pro Gly Ala Tyr Asn Phe Pro						
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220	tac tgc gaa gct ggc tct tgc cac cct gcc ggt ctg gcc cca gtg gat	2269					
221	Tyr Cys Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Val Asp						
222		720		725		730	
224	cct gcc ctt cct gag gca cag gtt ccc tgt atg tgc cgg gct cac gtg	2317					
225	Pro Ala Leu Pro Glu Ala Gln Val Pro Cys Met Cys Arg Ala His Val						
226	735		740		745		750
228	gag ggg ccg agc tgt gac cgc tgc aaa cct ggg ttc tgg gga ctg agc	2365					
229	Glu Gly Pro Ser Cys Asp Arg Cys Lys Pro Gly Phe Trp Gly Leu Ser						
230		755		760		765	
232	ccc agc aac ccc gag ggc tgt acc cgc tgc agc tgc gac ctc agg ggc	2413					
233	Pro Ser Asn Pro Glu Gly Cys Thr Arg Cys Ser Cys Asp Leu Arg Gly						
234		770		775		780	
236	aca ctg ggt gga gtt gct gag tgc cag ccg ggc acc ggc cag tgc ttc	2461					
237	Thr Leu Gly Gly Val Ala Glu Cys Gln Pro Gly Thr Gly Gln Cys Phe						
238		785		790		795	
240	tgc aag ccc cac gtg tgc ggc cag gcc tgc gcg tcc tgc aag gat ggc	2509					
241	Cys Lys Pro His Val Cys Gly Gln Ala Cys Ala Ser Cys Lys Asp Gly						
242		800		805		810	
244	ttc ttt gga ctg gat cag gct gac tat ttt ggc tgc cgc agc tgc cgg	2557					
245	Phe Phe Gly Leu Asp Gln Ala Asp Tyr Phe Gly Cys Arg Ser Cys Arg						
246	815		820		825		830
248	tgt gac att ggc ggt gca ctg ggc cag agc tgt gaa ccg agg acg ggc	2605					
249	Cys Asp Ile Gly Gly Ala Leu Gly Gln Ser Cys Glu Pro Arg Thr Gly						
250		835		840		845	
252	gtc tgc cgg tgc cgc ccc aac acc cag ggc ccc acc tgc agc gag cct	2653					
253	Val Cys Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro						
254		850		855		860	
256	gcg agg gac cac tac ctc ccg gac ctg cac cac ctg cgc ctg gag ctg	2701					
257	Ala Arg Asp His Tyr Leu Pro Asp Leu His His Leu Arg Leu Glu Leu						
258		865		870		875	

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260	gag	gag	gct	gcc	aca	cct	gag	ggt	cac	gcc	gtg	cgc	ttt	ggc	ttc	aac	2749
261	Glu	Glu	Ala	Ala	Thr	Pro	Glu	Gly	His	Ala	Val	Arg	Phe	Gly	Phe	Asn	
262		880						885				890					
264	ccc	ctc	gag	ttc	gag	aac	ttc	agc	tgg	agg	ggc	tac	gcg	cag	atg	gca	2797
265	Pro	Leu	Glu	Phe	Glu	Asn	Phe	Ser	Trp	Arg	Gly	Tyr	Ala	Gln	Met	Ala	
266	895					900					905					910	
268	cct	gtc	cag	ccc	agg	atc	gtg	gcc	agg	ctg	aac	ctg	acc	tcc	ccc	gac	2845
269	Pro	Val	Gln	Pro	Arg	Ile	Val	Ala	Arg	Leu	Asn	Leu	Thr	Ser	Pro	Asp	
270					915					920					925		
272	ctt	ttc	tgg	ctc	gtc	ttc	cga	tac	gtc	aac	cgg	ggg	gcc	atg	agt	gtg	2893
273	Leu	Phe	Trp	Leu	Val	Phe	Arg	Tyr	Val	Asn	Arg	Gly	Ala	Met	Ser	Val	
274				930					935				940				
276	agc	ggg	cgg	gtc	tct	gtg	cga	gag	gag	ggc	agg	tcg	gcc	gcc	tgt	gcc	2941
277	Ser	Gly	Arg	Val	Ser	Val	Arg	Glu	Glu	Gly	Arg	Ser	Ala	Ala	Cys	Ala	
278			945					950					955				
280	aac	tgc	aca	gca	cag	agt	cag	ccc	gtg	gcc	ttc	cca	ccc	agc	acg	gag	2989
281	Asn	Cys	Thr	Ala	Gln	Ser	Gln	Pro	Val	Ala	Phe	Pro	Pro	Ser	Thr	Glu	
282		960						965				970					
284	cct	gcc	ttc	atc	acc	gtg	ccc	cag	agg	ggc	ttc	gga	gag	ccc	ttt	gtg	3037
285	Pro	Ala	Phe	Ile	Thr	Val	Pro	Gln	Arg	Gly	Phe	Gly	Glu	Pro	Phe	Val	
286	975					980				985						990	
288	ctg	aac	cct	ggc	acc	tgg	gcc	ctg	cgt	gtg	gag	gcc	gaa	ggg	gtg	ctc	3085
289	Leu	Asn	Pro	Gly	Thr	Trp	Ala	Leu	Arg	Val	Glu	Ala	Glu	Gly	Val	Leu	
290					995				1000					1005			
292	ctg	gac	tac	gtg	gtt	ctg	ctg	cct	agc	gca	tac	tac	gag	gcg	gcg	ctc	3133
293	Leu	Asp	Tyr	Val	Val	Leu	Leu	Pro	Ser	Ala	Tyr	Tyr	Glu	Ala	Ala	Leu	
294				1010					1015				1020				
296	ctg	cag	ctg	cgg	gtg	act	gag	gcc	tgc	aca	tac	cgt	ccc	tct	gcc	cag	3181
297	Leu	Gln	Leu	Arg	Val	Thr	Glu	Ala	Cys	Thr	Tyr	Arg	Pro	Ser	Ala	Gln	
298			1025					1030				1035					
300	cag	tct	ggc	gac	aac	tgc	ctc	ctc	tac	aca	cac	ctc	ccc	ctg	gat	ggc	3229
301	Gln	Ser	Gly	Asp	Asn	Cys	Leu	Leu	Tyr	Thr	His	Leu	Pro	Leu	Asp	Gly	
302		1040					1045					1050					
304	ttc	ccc	tcg	gcc	gcc	ggg	ctg	gag	gcc	ctg	tgt	cgc	cag	gac	aac	agc	3277
305	Phe	Pro	Ser	Ala	Ala	Gly	Leu	Glu	Ala	Leu	Cys	Arg	Gln	Asp	Asn	Ser	
306	1055				1060				1065						1070		
308	ctg	ccc	cgg	ccc	tgc	ccc	acg	gag	cag	ctc	agc	ccg	tcg	cac	ccg	cca	3325
309	Leu	Pro	Arg	Pro	Cys	Pro	Thr	Glu	Gln	Leu	Ser	Pro	Ser	His	Pro	Pro	
310					1075				1080					1085			
312	ctg	atc	acc	tgc	acg	ggc	agt	gat	gtg	gac	gtc	cag	ctt	caa	gtg	gca	3373
313	Leu	Ile	Thr	Cys	Thr	Gly	Ser	Asp	Val	Asp	Val	Gln	Leu	Gln	Val	Ala	
314				1090					1095					1100			
316	gtg	cca	cag	cca	ggc	cgc	tat	gcc	cta	gtg	gtg	gag	tac	gcc	aat	gag	3421
317	Val	Pro	Gln	Pro	Gly	Arg	Tyr	Ala	Leu	Val	Val	Glu	Tyr	Ala	Asn	Glu	
318			1105					1110				1115					
320	gat	gcc	cgc	cag	gag	gtg	ggc	gtg	gct	gtg	cac	acc	cca	cag	cgg	gcc	3469
321	Asp	Ala	Arg	Gln	Glu	Val	Gly	Val	Ala	Val	His	Thr	Pro	Gln	Arg	Ala	
322		1120					1125				1130						
324	ccc	cag	cag	ggg	ctg	ctc	tcc	ctg	cac	ccc	tgc	ctg	tac	agc	acc	ctg	3517

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date